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Topology and dynamics of gene regulatory networks: a meta-analysis

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Topology and dynamics of gene regulatory networks: a meta-analysis

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Gene regulatory networks (GRNs), frequently modeled using Boolean networks, describe how a collection of genes governs the processes within a cell. Boolean networks are intuitive, simple to describe, and yield qualitative results even given sparse data. The biological term canalization reflects a cell's ability to maintain a stable phenotype despite ongoing environmental perturbations. Accordingly, Boolean canalizing functions are functions where the output is already determined if a certain, canalizing variable takes on its canalizing input, regardless of all other inputs. Due to their biological meaningfulness, this class of functions has been hypothesized to be overrepresented in GRNs and used as an explanation for the observed stability of GRNs; however, published GRNs have never been properly evaluated to test this hypothesis.

Using text- and data-mining techniques and the PubMed search engine, we generated an expandable database of published Boolean GRNs, and extracted the rules governing these networks. A meta-analysis of all extracted curated rules confirmed a strong overrepresentation of certain types of canalizing functions. We further studied the relationship between network topology, stability and limit behavior and found significant differences between the published GRNs but also when comparing to random networks. These findings highlight how our continuously-expanding database provides a versatile tool for various meta-analyses.